CEN5021 NP SEQ LIST 09-10-04.txt
SEQUENCE LISTING

<110>   Mercken, Marc; Benson, Jacqueline M.

<120>   ANTI-AMYLOID ANTIBODIES, COMPOSITIONS, METHODS AND USES

<130>   CEN5021 NP

<140>   US 10/810,881
<141>   2004-03-26

<150>   US 60/458,474
<151>   2003-03-28

<150>   US 60/458,469
<151>   2003-03-28

<150>   US 60/458,509
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<170>   PatentIn version 3.3

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Gln Val Gln Leu Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly
1   5   10   15

Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Xaa
              20   25   30

Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Xaa Arg
          35   40   45

Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Ala Tyr Met Glu Leu
    50   55   60

Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Xaa
65   70   75   80

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Ser Thr Lys Gly
                85   90   95

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
              100   105   110

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro
        115   120   125

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Gln Ile Thr Leu Lys Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
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Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Xaa Trp
            20   25   30

Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu Trp Leu Ala Xaa Arg Leu
            35   40   45

Thr Ile Thr Lys Asp Thr Ser Lys Asn Gln Val Val Leu Thr Met Thr
        50   55   60

Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Xaa Trp
65   70   75   80

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Pro Thr Ser Pro
                85   90   95

Lys Val Phe Pro Leu Ser Leu Ser Ser Lys Ser Thr Ser Gly Gly Thr
                100   105   110

Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro
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Glu Val Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
1   5   10   15

Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Xaa
        20   25   30

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Xaa Arg
        35   40   45

Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met
    50   55   60

Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Xaa
65   70   75   80

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Ser Thr Lys Ala
                85   90   95

Pro Ser Val Phe
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1				5					10					15	

Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Xaa	Trp
			20					25					30		

Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	Gly	Xaa	Arg	Phe
		35					40					45			

Thr	Ile	Ser	Arg	Asp	Asp	Ser	Lys	Asn	Thr	Leu	Tyr	Leu	Gln	Met	Asn
	50					55					60				

Ser	Leu	Lys	Thr	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Thr	Thr	Xaa	Trp
65					70					75					80

Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro
				85					90					95	

Ser	Val	Phe	Pro	Leu	Ala
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Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1               5               10              15

Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Thr Phe Gly Xaa Trp
            20              25              30

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Gly Xaa Arg Phe
        35              40              45

Thr Ile Ser Arg Asp Asp Ser Lys Ser Ile Ala Tyr Leu Gln Met Asn
    50              55              60

Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Thr Arg Asn Xaa
65              70              75              80

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Ser Thr Lys Gly
            85              90              95

Pro Ser Val Leu Pro
            100
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Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1   5   10   15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ser Ile Ser Ser
            20   25   30

Ser Xaa Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly
        35   40   45

Xaa Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
    50   55   60

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
65   70   75   80

Arg Xaa Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Pro Thr
        85   90   95

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Lys Ala Pro Asp Val Phe Pro Ile Ile Ser Gly Cys
            100                 105
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Glu Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly
1               5                   10                  15


Glu Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Xaa
            20                  25                  30
```

Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met Gly Xaa Gln
     35   40   45

Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu Gln Trp
     50   55   60

Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala Arg Xaa
65   70   75   80

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Ala
          85   90   95

Pro Ser Val Phe Pro Leu Val Ser Cys Glu Asn Ser Pro Ser Asp Thr
         100   105   110

Ser Ser Val Ala Val Gly Cys Leu Ala Gln Asp Phe Leu Pro Asp Ser
         115   120   125

Ile Thr Phe Ser
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Gln Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1   5   10   15

Thr Leu Ser Leu Thr Cys Ala Ile Ser Gly Asp Ser Val Ser Xaa Trp
            20   25   30

Ile Arg Gln Ser Pro Ser Arg Gly Leu Glu Trp Leu Gly Xaa Arg Ile
            35   40   45

Thr Ile Asn Pro Asp Thr Ser Lys Asn Gln Phe Ser Leu Gln Leu Asn
        50   55   60

Ser Val Thr Pro Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Xaa Trp
65   70   75   80

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Ser Ala Ser Ala Pro
                85   90   95

Thr Leu Phe Pro Leu Val Ser Cys Glu Asn Ser Pro Ser Asp Thr Ser
            100   105   110

Ser Val Ala Val Gly Cys Leu Ala Gln Asp Phe Leu Pro
            115   120   125

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Gln Val Gln Leu Val Gln Ser Gly Ser Glu Leu Lys Lys Pro Gly Ala
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Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Xaa Trp
            20   25   30

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Xaa Arg Phe
        35   40   45

Val Phe Ser Leu Asp Thr Ser Val Ser Thr Ala Tyr Leu Gln Ile Ser
    50   55   60

Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Xaa Trp
65   70   75   80

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ser
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Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
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Asp Arg Arg Val Thr Ile Thr Cys Xaa Trp Tyr Gln Gln Lys Pro Gly
                20   25   30

Lys Ala Pro Lys Leu Leu Ile Tyr Xaa Gly Val Pro Ser Arg Phe Ser
            35   40   45

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln

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       50                    55                   60
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Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Xaa Phe Gly Gln Gly Thr Lys
65                  70                  75                  80
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Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe
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Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
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1                 5                 10                 15

Gln Pro Ala Ser Ile Ser Cys Xaa Trp Tyr Leu Gln Lys Pro Gly Gln
        20                  25                  30

Ser Pro Gln Leu Leu Ile Tyr Xaa Gly Val Pro Asp Arg Phe Ser Gly
        35                  40                  45

Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala
    50                  55                  60

Glu Asp Val Gly Val Tyr Tyr Cys Xaa Phe Gly Gln Gly Thr Lys Val
65                  70                  75                  80

Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe
                85                  90
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Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1   5   10   15

Glu Arg Ala Thr Leu Ser Cys Xaa Trp Tyr Gln Gln Lys Pro Gly Gln
            20   25   30

Ala Pro Arg Leu Leu Ile Tyr Xaa Gly Ile Pro Asp Arg Phe Ser Gly
        35   40   45

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro
    50   55   60

Glu Asp Phe Ala Val Tyr Tyr Cys Xaa Phe Gly Gln Gly Thr Lys Val
65   70   75   80

Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val
            85   90

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<400>   13
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Glu Thr Thr Leu Thr Gln Ser Pro Ala Phe Met Ser Ala Thr Pro Gly
1   5   10   15

Asp Lys Val Asn Ile Ser Cys Xaa Trp Tyr Gln Gln Lys Pro Gly Glu
            20   25   30

Ala Ala Ile Phe Ile Ile Gln Xaa Gly Ile Pro Pro Arg Phe Ser Gly
            35   40   45

Ser Gly Tyr Gly Thr Asp Phe Thr Leu Thr Ile Asn Asn Ile Glu Ser
    50   55   60

Glu Asp Ala Ala Tyr Tyr Phe Cys Xaa Leu Arg His Phe Trp Pro Gly
65   70   75   80

Asp Gln Ala Ala Gly
                85

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<223>   framework 1
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<223>  framework 2

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<223>  framework 3

<220>
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<223>  framework 4

<400>  14

Glu Ile Val Met Thr Gln Ser Pro Val Asn Leu Ser Met Ser Ala Gly
1               5                   10                  15


Glu Xaa Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Phe Ile
        20                  25                  30


Tyr Xaa Gly Ile Ser Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
        35                  40                  45


Phe Thr Leu Thr Ile Thr Ser Leu Gln Ser Glu Asp Phe Ala Val Tyr
    50                  55                  60


Tyr Cys Xaa Phe Gly Gln Gly Thr Lys Leu Asp Ile Lys Arg Thr
65                  70                  75


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<211>  77
<212>  PRT
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<223>  framework 1

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<223>  complementarity determinng region 1 (CDR1), X is 10-30 (18) of
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<223>  framework 2

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<223>  framework 3

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<223>  framework 4

<400>  15
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Glu Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Xaa
1   5   10   15

Trp Tyr Gln His Lys Pro Gly Gln Ala Pro Arg Leu Val Ile His Xaa
            20   25   30

Gly Ile Ser Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
        35   40   45

Leu Thr Ile Thr Arg Leu Glu Pro Glu Asp Phe Ala Leu Tyr Tyr Cys
    50   55   60

Xaa Phe Gly Gln Gly Thr Lys Leu Asp Phe Lys Arg Thr
65   70   75

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<210>  16
<211>  98
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<223>  complementarity determinng region 1 (CDR1). X is 5-25 (14) of any
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<220>
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<223>  framework 2

<220>
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<223>  framework 3

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<223>  complementarity determinng region 3 (CDR3). X is 30-50 (39) of
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<220>
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<223>  framework 4

<400>  16

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1               5                   10                  15


Arg Val Thr Ile Ser Cys Xaa Trp Tyr Gln Gln Leu Pro Gly Thr Ala
            20                  25                  30


Pro Lys Leu Leu Ile Tyr Xaa Gly Val Pro Asp Arg Phe Ser Gly Ser
        35                  40                  45
```

Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln Ser Glu
    50   55   60

Asp Glu Ala Asp Tyr Tyr Cys Xaa Phe Gly Gly Gly Thr Lys Leu Thr
65   70   75   80

Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro
            85   90   95

Ser Ser

<210>   17
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<223>   framework 1

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<223>   complementarity determinng region 1 (CDR1), X is 3-25 (13) of any
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<223>   framework 2

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<223>   framework 3

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<223>   framework 4

<400>   17

Ala Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Ala Ala Pro Gly
1   5   10   15

Gln Lys Val Thr Ile Ser Cys Xaa Trp Tyr Gln Gln Leu Pro Gly Thr
            20   25   30

Ala Pro Lys Leu Leu Ile Tyr Xaa Gly Ile Pro Asp Arg Phe Ser Gly
        35   40   45

Ser Lys Ser Gly Thr Ser Ala Thr Leu Gly Ile Thr Gly Leu Gln Thr
    50   55   60

Gly Asp Glu Ala Asp Tyr Tyr Cys Xaa Phe Gly Gly Gly Thr Lys Leu
65   70   75   80

Thr Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro
            85   90   95

Pro Ser Ser

<210>   18
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<223>   framework 1

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<223>   complementarity determinng region 1 (CDR1), X is 8-25 (14) of any
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<223>   framework 2

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amino acids.

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<223>  framework 4

<400>  18
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Gln Ser Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln
1   5   10   15

Ser Ile Thr Ile Ser Cys Xaa Trp Tyr Gln Gln His Pro Gly Lys Ala
            20   25   30

Pro Lys Leu Met Ile Tyr Xaa Gly Val Ser Asn Arg Phe Ser Gly Ser
        35   40   45

Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu Gln Ala Glu
    50   55   60

Asp Glu Ala Asp Tyr Tyr Cys Xaa Phe Gly Gly Gly Thr Thr Lys Leu
65   70   75   80

Thr Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro
                85   90   95

Pro Ser Ser

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<213>  Homo sapiens

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<223>  framework 3

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<223>  framework 4

<400>  19
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Ser Tyr Glu Leu Thr Gln Pro Pro Ser Val Ser Val Ser Pro Gly Gln
1   5   10   15

Thr Ala Arg Ile Thr Cys Xaa Trp Tyr Gln Gln Lys Pro Gly Gln Ala
            20   25   30

Pro Val Leu Val Ile Tyr Xaa Gly Ile Pro Glu Arg Phe Ser Gly Ser
        35   40   45

Ser Ser Gly Thr Thr Ala Thr Leu Thr Ile Ser Gly Val Gln Ala Glu
    50   55   60

Asp Glu Ala Asp Tyr Tyr Cys Xaa Phe Gly Gly Gly Thr Lys Leu Thr
65   70   75   80

Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro
                85   90   95

Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr
            100   105

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<223>  framework 3

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<220>
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<223>  framework 4

<400>  20

Ser Tyr Val Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln
1               5                   10                  15


Thr Ala Arg Ile Thr Cys Xaa Trp Tyr Gln Gln Lys Pro Gly Gln Ala
                20                  25                  30


Pro Val Leu Val Val Tyr Asp Xaa Gly Ile Pro Glu Arg Phe Ser Gly
            35                  40                  45
```

Ser Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Arg Val Glu Ala
 50   55   60

Gly Asp Glu Ala Asp Tyr Tyr Cys Xaa Phe Gly Gly Gly Thr Lys Leu
65   70   75   80

Thr Val Leu Gly Gln Pro Lys Ala Ala Pro Thr Val Thr
                 85   90

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<223> framework 3

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<223> framework 4

<400> 21

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Ser Tyr Glu Leu Thr Gln Pro Pro Ser Val Ser Val Ser Pro Gly Gln
1               5                   10                  15


Thr Ala Ser Ile Thr Cys Xaa Trp Tyr Gln Gln Lys Pro Gly Gln Ser
                20              25              30


Pro Val Leu Val Ile Tyr Xaa Gly Ile Pro Glu Arg Phe Ser Gly Ser
            35              40              45


Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Met
    50              55              60


Asp Glu Ala Asp Tyr Tyr Cys Xaa Phe Gly Gly Gly Thr Lys Leu Thr
65              70              75                  80


Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Arg Ser Leu Cys Pro Pro
                85                  90                  95


Pro Pro
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<210> 22
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<213> Homo sapiens

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<223> framework 1

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<223>   framework 4

<400>   22
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Ser Ser Glu Leu Thr Gln Asp Pro Ala Val Ser Val Ala Leu Gly Gln
1   5   10   15

Thr Val Arg Ile Thr Cys Xaa Trp Tyr Gln Gln Lys Pro Gly Gln Ala
            20   25   30

Pro Val Leu Val Ile Tyr Xaa Gly Ile Pro Asp Arg Phe Ser Gly Ser
        35   40   45

Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu
    50   55   60

Asp Glu Ala Asp Tyr Tyr Cys Xaa Phe Gly Gly Gly Thr Lys Leu Thr
65   70   75   80

Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro
            85   90   95

Ser Ser

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<210>   23
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<213>   Homo sapiens

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<220>
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<223>   framework 2

<220>
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        amino acids.

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<223>   framework 3

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<220>
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<223>   framework 4

<400>   23
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Gln Pro Val Leu Thr Gln Ser Ser Ser Ala Ser Ala Ser Leu Gly Ser
1               5                   10                  15


Ser Val Lys Leu Thr Cys Xaa Trp His Gln Gln Pro Gly Lys Ala
                20                  25              30


Pro Arg Tyr Leu Met Lys Xaa Gly Val Pro Asp Arg Phe Ser Gly Ser
            35                  40                  45


Ser Ser Gly Ala Asp Arg Tyr Leu Thr Ile Ser Asn Leu Gln Ser Glu
        50                  55                  60


Asp Glu Ala Asp Tyr Tyr Cys Xaa Phe Gly Gly Gly Thr Lys Leu Thr
65                  70                  75                  80


Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe
                85                  90
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<213>   Homo sapiens
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<223>   complementarity determinng region 1 (CDR1), X is 5-25 (12) of any
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<223>   framework 2

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<223>   framework 3

<220>
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<222>   (73)..(95)
<223>   framework 4

<400>   24
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Gln Leu Val Leu Thr Gln Ser Pro Ser Ala Ser Ala Ser Leu Gly Ala
1   5   10   15

Ser Val Lys Leu Thr Cys Xaa Trp His Gln Gln Pro Glu Lys Gly
            20   25   30

Pro Arg Tyr Leu Met Lys Xaa Gly Ile Pro Asp Arg Phe Ser Gly Ser
            35   40   45

Ser Ser Gly Ala Glu Arg Tyr Leu Thr Ile Ser Ser Leu Gln Ser Glu
        50   55   60

Asp Glu Ala Asp Tyr Tyr Cys Xaa Phe Gly Gly Ile Gly Gly Gly Thr
65   70   75   80

```
Lys Leu Thr Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Ser
            85                  90                  95
```

<210> 25
<211> 88
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<213> Homo sapiens

<220>
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<223> Lambda5 light chain variable region

<220>
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<223> framework 1

<220>
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<223> complementarity determinng region 1 (CDR1), X is 5-25 (14) of any
      amino acids.

<220>
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<223> framework 2

<220>
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      amino acids.

<220>
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<223> framework 3

<220>
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<223> complementarity determinng region 3 (CDR3), X is 10-35 (22) of
      any amino acids.

<220>
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<223> framework 4

<400> 25

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Gln Ala Val Leu Thr Gln Pro Ser Ser Leu Ser Ala Ser Pro Gly Ala
1                   5                   10                  15


Ser Ala Ser Leu Thr Cys Xaa Trp Tyr Gln Gln Lys Pro Gly Ser Pro
            20                  25                  30
```

```
Pro Gln Tyr Leu Leu Arg Tyr Xaa Gly Val Pro Ser Arg Phe Ser Gly
        35                      40              45


Ser Lys Asp Ala Ser Ala Asn Ala Gly Ile Leu Leu Ile Ser Gly Leu
    50                  55                  60


Gln Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Xaa Phe Gly Gly Gly Thr
65                  70                  75                  80


Lys Leu Thr Val Leu Ser Gln Pro
                    85
```

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<210>   26
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<213>   Homo sapiens


<220>
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<223>   framewrok 1

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<223>   complementarity determinng region 1 (CDR1), X is 5-25 (13) of any
        amino acids.

<220>
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<223>   framewrok 2

<220>
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<223>   complementarity determinng region 2 (CDR2), X is 3-20 (7) of any
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<220>
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<223>   framewrok 3

<220>
<221>   MISC_FEATURE
<222>   (74)..(74)
<223>   complementarity determinng region 3 (CDR3), X is 25-50 (38) of
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<220>
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<223>   framewrok 4

<400>   26
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Asn Phe Met Leu Thr Gln Pro His Ser Val Ser Glu Ser Pro Gly Lys
1   5   10   15

Thr Val Thr Ile Ser Cys Xaa Trp Tyr Gln Gln Arg Pro Gly Ser Ala
                20   25   30

Pro Thr Thr Val Ile Tyr Xaa Gly Val Pro Asp Arg Phe Ser Gly Ser
            35   40   45

Ile Asp Ser Ser Ser Asn Ser Ala Ser Leu Thr Ile Ser Gly Leu Lys
        50   55   60

Thr Glu Asp Glu Ala Asp Tyr Tyr Cys Xaa Phe Gly Gly Gly Thr Lys
65   70   75   80

Leu Thr Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe
                85   90   95

Pro Pro Ser Ser Ser
            100

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<210>   27
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<213>   Homo sapiens


<220>
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<223>   Lambda7 light chain variable region

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<223>   framework 1

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<220>
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<223>   framework 2

<220>
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<222>  (39)..(39)
<223>  complementarity determinng region 2 (CDR2), X is 3-20 (7) of any
       amino acids.

<220>
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<223>  framework 3

<220>
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<222>  (72)..(72)
<223>  complementarity determinng region 3 (CDR3), X is 10-35 (23) of
       any amino acids.

<220>
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<222>  (73)..(89)
<223>  framework 4

<400>  27
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Gln Ala Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly
1   5   10   15

Thr Val Thr Leu Thr Cys Xaa Trp Phe Gln Gln Lys Pro Gly Gln Ala
            20   25   30

Pro Arg Ala Leu Ile Tyr Xaa Trp Thr Pro Ala Arg Phe Ser Gly Ser
        35   40   45

Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu
    50   55   60

Asp Glu Ala Glu Tyr Tyr Cys Xaa Phe Gly Gly Gly Thr Lys Leu Thr
65   70   75   80

Val Leu Gly Gln Pro Lys Ala Ala Pro
                85

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<210>  28
<211>  89
<212>  PRT
<213>  Homo sapiens


<220>
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<223>  Lambda8 light chain variable region

<220>
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<223>  framework 1

<220>
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<220>
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<223>   framework 2

<220>
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<223>   complementarity determinng region 2 (CDR2), X is 3-20 (7) of any
        amino acids.

<220>
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<223>   framework 3

<220>
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<223>   complementarity determinng region 3 (CDR3), X is 15-35 (25) of
        any amino acids.

<220>
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<223>   framework 4

<400>   28
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Gln Thr Val Val Thr Gln Glu Pro Ser Phe Ser Val Ser Pro Gly Gly
1   5   10   15

Thr Val Thr Leu Thr Cys Xaa Trp Tyr Gln Gln Thr Pro Gly Gln Ala
            20   25   30

Pro Arg Thr Leu Ile Tyr Xaa Gly Val Pro Asp Arg Phe Ser Gly Ser
        35   40   45

Ile Leu Gly Asn Lys Ala Ala Leu Thr Ile Thr Gly Ala Gln Ala Asp
    50   55   60

Asp Glu Ser Asp Tyr Tyr Cys Xaa Phe Gly Gly Gly Thr Lys Leu Thr
65   70   75   80

Val Leu Gly Gln Pro Lys Ala Ala Pro
                85

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<210>   29
<211>   91
<212>   PRT
<213>   Homo sapiens
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<223>    Lambda9 light chain variable region

<220>
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<223>    framework 1

<220>
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<223>    complementarity determinng region 1 (CDR1), X is 5-25 (12) of any
         amino acids.

<220>
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<223>    framework 2

<220>
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<223>    complementarity determinng region 2 (CDR2), X is 5-25 (12) of any
         amino acids.

<220>
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<223>    framework 3

<220>
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<223>    complementarity determinng region 3 (CDR3), X is 15-40 (28) of
         any amino acids.

<220>
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<223>    framework 4

<400>    29

Gln Pro Val Leu Thr Gln Pro Pro Ser Ala Ser Ala Ser Leu Gly Ala
1               5               10              15

Ser Val Thr Leu Thr Cys Xaa Trp Tyr Gln Gln Arg Pro Gly Lys Gly
                20              25              30

Pro Arg Phe Val Met Arg Xaa Gly Ile Pro Asp Arg Phe Ser Val Leu
        35              40              45

Gly Ser Gly Leu Asn Arg Tyr Leu Thr Ile Lys Asn Ile Gln Glu Glu
    50              55              60

Asp Glu Ser Asp Tyr His Cys Xaa Phe Gly Gly Gly Thr Lys Leu Thr
```

65   70   75   80

Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Val
              85   90

<210> 30
<211> 87
<212> PRT
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<223> Lambda10 light chain variable region

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<223> framework 1

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<223> complementarity determinng region 1 (CDR1), X is 5-25 (13) of any
      amino acids.

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<223> framework 2

<220>
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      amino acids.

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<223> framework 3

<220>
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<223> complementarity determinng region 3 (CDR3), X is 15-40 (27) of
      any amino acids.

<220>
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<223> framework 4

<400> 30

Gln Ala Gly Leu Thr Gln Pro Pro Ser Val Ser Lys Gly Leu Arg Gln
1   5   10   15

Thr Ala Thr Leu Thr Cys Xaa Trp Leu Gln Gln His Gln Gly His Pro

                20   25   30

Pro Lys Leu Leu Ser Tyr Xaa Gly Ile Ser Glu Arg Phe Ser Ala Ser
         35   40   45

Arg Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Leu Gln Pro Glu
         50   55   60

Asp Glu Ala Asp Tyr Tyr Cys Xaa Phe Gly Gly Gly Thr Lys Leu Thr
65   70   75   80

Val Leu Gly Gln Pro Lys Ala
                85

<210>   31
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<212>   PRT
<213>   Homo sapiens

<220>
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<223>   IgA1 heavy chain constant region

<220>
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<223>   CH1

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<223>   hinge

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<223>   CH2

<220>
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<222>   (223)..(354)
<223>   CH3

<400>   31

Ala Ser Pro Thr Ser Pro Lys Val Phe Pro Leu Ser Leu Cys Ser Thr
1   5   10   15

Gln Pro Asp Gly Asn Val Val Ile Ala Cys Leu Val Gln Gly Phe Phe
                20   25   30

Pro Gln Glu Pro Leu Ser Val Thr Trp Ser Glu Ser Gly Gln Gly Val
         35   40   45

Thr Ala Arg Asn Phe Pro Pro Ser Gln Asp Ala Ser Gly Asp Leu Tyr
 50   55   60

Thr Thr Ser Ser Gln Leu Thr Leu Pro Ala Thr Gln Cys Leu Ala Gly
65   70   75   80

Lys Ser Val Thr Cys His Val Lys His Tyr Thr Asn Pro Ser Gln Asp
            85   90   95

Val Thr Val Pro Cys Pro Val Pro Ser Thr Pro Pro Thr Pro Ser Pro
            100   105   110

Ser Thr Pro Pro Thr Pro Ser Pro Ser Cys Cys His Pro Arg Leu Ser
    115   120   125

Leu His Arg Pro Ala Leu Glu Asp Leu Leu Leu Gly Ser Glu Ala Asn
    130   135   140

Leu Thr Cys Thr Leu Thr Gly Leu Arg Asp Ala Ser Gly Val Thr Phe
145   150   155   160

Thr Trp Thr Pro Ser Ser Gly Lys Ser Ala Val Gln Gly Pro Pro Glu
            165   170   175

Arg Asp Leu Cys Gly Cys Tyr Ser Val Ser Ser Val Leu Pro Gly Cys
            180   185   190

Ala Glu Pro Trp Asn His Gly Lys Thr Phe Thr Cys Thr Ala Ala Tyr
    195   200   205

Pro Glu Ser Lys Thr Pro Leu Thr Ala Thr Leu Ser Lys Ser Gly Asn
    210   215   220

Thr Phe Arg Pro Glu Val His Leu Leu Pro Pro Pro Ser Glx Glu Glu
225   230   235   240

Leu Ala Leu Asn Glu Leu Val Thr Leu Thr Cys Leu Ala Arg Gly Phe
            245   250   255

Ser Pro Lys Asp Val Leu Val Arg Trp Leu Gln Gly Ser Gln Glu Leu
            260   265   270

Pro Arg Glu Lys Tyr Leu Thr Trp Ala Ser Arg Gln Glu Pro Ser Gln
    275   280   285

Gly Thr Thr Thr Phe Ala Val Thr Ser Ile Leu Arg Val Ala Ala Glu
    290   295   300

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```
Asp Trp Lys Lys Gly Asp Thr Phe Ser Cys Met Val Gly His Glu Ala
305             310             315             320


Leu Pro Leu Ala Phe Thr Gln Lys Thr Ile Asp Arg Leu Ala Gly Lys
            325             330             335


Pro Thr His Val Asn Val Ser Val Val Met Ala Glu Val Asp Gly Thr
            340             345             350


Cys Tyr
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<210>    32
<211>    340
<212>    PRT
<213>    Homo sapiens


<220>
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<223>    IgA2 heavy chain constant region

<220>
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<223>    CH1

<220>
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<223>    hinge

<220>
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<222>    (109)..(209)
<223>    CH2

<220>
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<222>    (210)..(340)
<223>    CH3

<400>    32
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Ala Ser Pro Thr Ser Pro Lys Val Phe Pro Leu Ser Leu Asp Ser Thr
1               5               10              15


Pro Gln Asp Gly Asn Val Val Val Ala Cys Leu Val Gln Gly Phe Phe
            20              25              30


Pro Gln Glu Pro Leu Ser Val Thr Trp Ser Glu Ser Gly Gln Asn Val
        35              40              45
```

```
Thr Ala Arg Asn Phe Pro Pro Ser Gln Asp Ala Ser Gly Asp Leu Tyr
 50              55              60

Thr Thr Ser Ser Gln Leu Thr Leu Pro Ala Thr Gln Cys Pro Asp Gly
 65              70              75              80

Lys Ser Val Thr Cys His Val Lys His Tyr Thr Asn Pro Ser Gln Asp
             85              90              95

Val Thr Val Pro Cys Pro Val Pro Pro Pro Pro Cys Cys His Pro
             100             105             110

Arg Leu Ser Leu His Arg Pro Ala Leu Glu Asp Leu Leu Leu Gly Ser
         115             120             125

Glu Ala Asn Leu Thr Cys Thr Leu Thr Gly Leu Arg Asp Ala Ser Gly
     130             135             140

Ala Thr Phe Thr Trp Thr Pro Ser Ser Gly Lys Ser Ala Val Gln Gly
 145             150             155             160

Pro Pro Glu Arg Asp Leu Cys Gly Cys Tyr Ser Val Ser Ser Val Leu
             165             170             175

Pro Gly Cys Ala Gln Pro Trp Asn His Gly Glu Thr Phe Thr Cys Thr
             180             185             190

Ala Ala His Pro Glu Leu Lys Thr Pro Leu Thr Ala Asn Ile Thr Lys
         195             200             205

Ser Gly Asn Thr Phe Arg Pro Glu Val His Leu Leu Pro Pro Pro Ser
 210             215             220

Glu Glu Leu Ala Leu Asn Glu Leu Val Thr Leu Thr Cys Leu Ala Arg
 225             230             235             240

Gly Phe Ser Pro Lys Asp Val Leu Val Arg Trp Leu Gln Gly Ser Gln
             245             250             255

Glu Leu Pro Arg Glu Lys Tyr Leu Thr Trp Ala Ser Arg Gln Glu Pro
             260             265             270

Ser Gln Gly Thr Thr Thr Phe Ala Val Thr Ser Ile Leu Arg Val Ala
         275             280             285

Ala Glu Asp Trp Lys Lys Gly Asp Thr Phe Ser Cys Met Val Gly His
 290             295             300
```

```
Glu Ala Leu Pro Leu Ala Phe Thr Gln Lys Thr Ile Asp Arg Leu Ala
305             310             315             320


Gly Lys Pro Thr His Val Asn Val Ser Val Val Met Ala Glu Val Asp
                325             330             335


Gly Thr Cys Tyr
            340
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<210>  33
<211>  384
<212>  PRT
<213>  Homo sapiens


<220>
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<223>  IgD heavy chain constant region

<220>
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<223>  CH1

<220>
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<222>  (102)..(135)
<223>  hinge 1

<220>
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<223>  hinge 2

<220>
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<223>  CH2

<220>
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<222>  (268)..(384)
<223>  CH3

<400>  33
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Ala Pro Thr Lys Ala Pro Asp Val Phe Pro Ile Ile Ser Gly Cys Arg
1               5               10              15


His Pro Lys Asp Asn Ser Pro Val Val Leu Ala Cys Leu Ile Thr Gly
                20              25              30


Tyr His Pro Thr Ser Val Thr Val Thr Trp Tyr Met Gly Thr Gln Ser
        35              40              45
```

Gln Pro Gln Arg Thr Phe Pro Glu Ile Gln Arg Arg Asp Ser Tyr Tyr
    50   55   60

Met Thr Ser Ser Gln Leu Ser Thr Pro Leu Gln Gln Trp Arg Gln Gly
65   70   75   80

Glu Tyr Lys Cys Val Val Gln His Thr Ala Ser Lys Ser Lys Lys Glu
            85   90   95

Ile Phe Arg Trp Pro Glu Ser Pro Lys Ala Gln Ala Ser Ser Val Pro
            100   105   110

Thr Ala Gln Pro Gln Ala Glu Gly Ser Leu Ala Lys Ala Thr Thr Ala
        115   120   125

Pro Ala Thr Thr Arg Asn Thr Gly Arg Gly Gly Glu Glu Lys Lys Lys
    130   135   140

Glu Lys Glu Lys Glu Glu Gln Glu Glu Arg Glu Thr Lys Thr Pro Glu
145   150   155   160

Cys Pro Ser His Thr Gln Pro Leu Gly Val Tyr Leu Leu Thr Pro Ala
            165   170   175

Val Gln Asp Leu Trp Leu Arg Asp Lys Ala Thr Phe Thr Cys Phe Val
        180   185   190

Val Gly Ser Asp Leu Lys Asp Ala His Leu Thr Trp Glu Val Ala Gly
        195   200   205

Lys Val Pro Thr Gly Gly Val Glu Glu Gly Leu Leu Glu Arg His Ser
    210   215   220

Asn Gly Ser Gln Ser Gln His Ser Arg Leu Thr Leu Pro Arg Ser Leu
225   230   235   240

Trp Asn Ala Gly Thr Ser Val Thr Cys Thr Leu Asn His Pro Ser Leu
            245   250   255

Pro Pro Gln Arg Leu Met Ala Leu Arg Glu Pro Ala Ala Gln Ala Pro
            260   265   270

Val Lys Leu Ser Leu Asn Leu Leu Ala Ser Ser Asp Pro Pro Glu Ala
        275   280   285

Ala Ser Trp Leu Leu Cys Glu Val Ser Gly Phe Ser Pro Pro Asn Ile
    290   295   300

Page 43

```
Leu Leu Met Trp Leu Glu Asp Gln Arg Glu Val Asn Thr Ser Gly Phe
305             310             315             320

Ala Pro Ala Arg Pro Pro Pro Gln Pro Arg Ser Thr Thr Phe Trp Ala
            325             330             335

Trp Ser Val Leu Arg Val Pro Ala Pro Pro Ser Pro Gln Pro Ala Thr
            340             345             350

Tyr Thr Cys Val Val Ser His Glu Asp Ser Arg Thr Leu Leu Asn Ala
        355             360             365

Ser Arg Ser Leu Glu Val Ser Tyr Val Thr Asp His Gly Pro Met Lys
    370             375             380
```

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<210>   34
<211>   497
<212>   PRT
<213>   Homo sapiens


<220>
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<223>   IgE heavy chain constant region

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<223>   CH1

<220>
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<223>   CH2

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<222>   (211)..(318)
<223>   CH3

<220>
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<222>   (319)..(497)
<223>   CH4

<400>   34
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Ala Ser Thr Gln Ser Pro Ser Val Phe Pro Leu Thr Arg Cys Cys Lys
1               5               10              15

Asn Ile Pro Ser Asn Ala Thr Ser Val Thr Leu Gly Cys Leu Ala Thr
            20              25              30

Gly Tyr Phe Pro Glu Pro Val Met Val Thr Trp Asp Thr Gly Ser Leu
```

                35   40   45

Asn Gly Thr Thr Met Thr Leu Pro Ala Thr Thr Leu Thr Leu Ser Gly
    50   55   60

His Tyr Ala Thr Ile Ser Leu Leu Thr Val Ser Gly Ala Trp Ala Lys
65   70   75   80

Gln Met Phe Thr Cys Arg Val Ala His Thr Pro Ser Ser Thr Asp Trp
            85   90   95

Val Asp Asn Lys Thr Phe Ser Val Cys Ser Arg Asp Phe Thr Pro Pro
            100   105   110

Thr Val Lys Ile Leu Gln Ser Ser Cys Asp Gly Gly Gly His Phe Pro
        115   120   125

Pro Thr Ile Gln Leu Leu Cys Leu Val Ser Gly Tyr Thr Pro Gly Thr
    130   135   140

Ile Asn Ile Thr Trp Leu Glu Asp Gly Gln Val Met Asp Val Asp Leu
145   150   155   160

Ser Thr Ala Ser Thr Thr Gln Glu Gly Glu Leu Ala Ser Thr Gln Ser
            165   170   175

Glu Leu Thr Leu Ser Gln Lys His Trp Leu Ser Asp Arg Thr Tyr Thr
            180   185   190

Cys Gln Val Thr Tyr Gln Gly His Thr Phe Glu Asp Ser Thr Lys Lys
        195   200   205

Cys Ala Asp Ser Asn Pro Arg Gly Val Ser Ala Tyr Leu Ser Arg Pro
    210   215   220

Ser Pro Phe Asp Leu Phe Ile Arg Lys Ser Pro Thr Ile Thr Cys Leu
225   230   235   240

Val Val Asp Leu Ala Pro Ser Lys Gly Thr Val Asn Leu Thr Trp Ser
            245   250   255

Arg Ala Ser Gly Lys Pro Val Asn His Ser Thr Arg Lys Glu Glu Lys
            260   265   270

Gln Arg Asn Gly Thr Leu Thr Val Thr Ser Thr Leu Pro Val Gly Thr
        275   280   285

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Arg Asp Trp Ile Glu Gly Glu Thr Tyr Gln Cys Arg Val Thr His Pro
    290   295   300

His Leu Pro Arg Ala Leu Met Arg Ser Thr Thr Lys Thr Ser Gly Pro
305   310   315   320

Val Gly Pro Arg Ala Ala Pro Glu Val Tyr Ala Phe Ala Thr Pro Glu
                325   330   335

Trp Pro Gly Ser Arg Asp Lys Arg Thr Leu Ala Cys Leu Ile Gln Asn
            340   345   350

Phe Met Pro Glu Asp Ile Ser Val Gln Trp Leu His Asn Glu Val Gln
        355   360   365

Leu Pro Asp Ala Arg His Ser Thr Thr Gln Pro Arg Lys Thr Lys Gly
    370   375   380

Ser Gly Phe Phe Val Phe Ser Arg Leu Glu Val Thr Arg Ala Glu Trp
385   390   395   400

Glu Gln Lys Asp Glu Phe Ile Cys Arg Ala Val His Glu Ala Ala Ser
            405   410   415

Pro Ser Gln Thr Val Gln Arg Ala Val Ser Val Asn Pro Gly Lys Asp
            420   425   430

Val Cys Val Glu Glu Ala Glu Gly Glu Ala Pro Trp Thr Trp Thr Gly
        435   440   445

Leu Cys Ile Phe Ala Ala Leu Phe Leu Leu Ser Val Ser Tyr Ser Ala
    450   455   460

Ala Leu Thr Leu Leu Met Val Gln Arg Phe Leu Ser Ala Thr Arg Gln
465   470   475   480

Gly Arg Pro Gln Thr Ser Leu Asp Tyr Thr Asn Val Leu Gln Pro His
            485   490   495

Ala

<210>   35
<211>   339
<212>   PRT
<213>   Homo sapiens

<220>

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<223>   IgG1 heavy chain constant region

<220>
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<223>   CH1

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<223>   hinge

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<223>   CH2

<220>
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<222>   (224)..(339)
<223>   CH3

<400>   35
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Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
1   5   10   15

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
                20   25   30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
            35   40   45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
        50   55   60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65   70   75   80

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
                85   90   95

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
                100   105   110

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
            115   120   125

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
        130   135   140

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp

145   150   155   160

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
              165   170   175

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
              180   185   190

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
              195   200   205

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
    210   215   220

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
225   230   235   240

Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
              245   250   255

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asx Asn Gly Gln Pro Glu
              260   265   270

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
              275   280   285

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
    290   295   300

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
305   310   315   320

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Thr His Thr Cys Pro
              325   330   335

Pro Cys Pro

<210> 36
<211> 326
<212> PRT
<213> Homo sapiens

<220>
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<220>

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<223>  CH1

<220>
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<223>  hinge

<220>
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<223>  CH2

<220>
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<223>  CH3

<400>  36
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Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
1   5   10   15

Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
            20   25   30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
        35   40   45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
    50   55   60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr
65   70   75   80

Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
                85   90   95

Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro
            100   105   110

Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
        115   120   125

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
    130   135   140

Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly
145   150   155   160

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn
                165   170   175

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Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp
        180   185   190

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro
        195   200   205

Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu
    210   215   220

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
225   230   235   240

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
            245   250   255

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
        260   265   270

Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
        275   280   285

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
    290   295   300

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
305   310   315   320

Ser Leu Ser Pro Gly Lys
            325

<210> 37
<211> 377
<212> PRT
<213> Homo sapiens

<220>
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<223> IgG3 heavy chain constant region

<220>
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<223> CH1

<220>
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<223> hinge 1

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<220>
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<223>   hinge 3

<220>
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<223>   hinge 4

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<223>   CH2

<220>
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<223>   CH3

<400>   37
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Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
1   5   10   15

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
                20   25   30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
            35   40   45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
        50   55   60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65   70   75   80

Tyr Thr Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
                85   90   95

Arg Val Glu Leu Lys Thr Pro Leu Gly Asp Thr Thr His Thr Cys Pro
                100   105   110

Arg Cys Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Cys Pro Arg
            115   120   125

Cys Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys
        130   135   140

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Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro
145              150              155              160


Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
            165              170              175


Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            180              185              190


Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Lys Trp Tyr
            195              200              205


Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    210              215              220


Gln Tyr Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Leu His
225              230              235              240


Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
            245              250              255


Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln
            260              265              270


Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
    275              280              285


Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
    290              295              300


Ser Asp Ile Ala Val Glu Trp Glu Ser Ser Gly Gln Pro Glu Asn Asn
305              310              315              320


Tyr Asn Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu
            325              330              335


Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Ile
            340              345              350


Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn Arg Phe Thr Gln
            355              360              365


Lys Ser Leu Ser Leu Ser Pro Gly Lys
    370              375
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<210> 38
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<223> CH3

<400> 38

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
1   5   10   15

Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
            20   25   30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
        35   40   45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
    50   55   60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr
65   70   75   80

Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
                85   90   95

Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro
            100   105   110

Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
        115   120   125

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val

    130   135   140

Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp
145   150   155   160

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe
                165   170   175

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
                180   185   190

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu
        195   200   205

Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
        210   215   220

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys
225   230   235   240

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
                245   250   255

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
                260   265   270

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
                275   280   285

Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser
        290   295   300

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
305   310   315   320

Leu Ser Leu Ser Leu Gly Lys
                325

<210>   39
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<213>   Homo sapiens

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<223>   IgM heavy chain constant region

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<223>   CH2

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Gly Ser Ala Ser Ala Pro Thr Leu Phe Pro Leu Val Ser Cys Glu Asn
1   5   10   15

Ser Pro Ser Asp Thr Ser Ser Val Ala Val Gly Cys Leu Ala Gln Asp
            20   25   30

Phe Leu Pro Asp Ser Ile Thr Phe Ser Trp Lys Tyr Lys Asn Asn Ser
            35   40   45

Asp Ile Ser Ser Thr Arg Gly Phe Pro Ser Val Leu Arg Gly Gly Lys
    50   55   60

Tyr Ala Ala Thr Ser Gln Val Leu Leu Pro Ser Lys Asp Val Met Gln
65   70   75   80

Gly Thr Asp Glu His Val Val Cys Lys Val Gln His Pro Asn Gly Asn
                85   90   95

Lys Glu Lys Asn Val Pro Leu Pro Val Ile Ala Glu Leu Pro Pro Lys
            100   105   110

Val Ser Val Phe Val Pro Pro Arg Asp Gly Phe Phe Gly Asn Pro Arg
            115   120   125

Ser Lys Ser Lys Leu Ile Cys Gln Ala Thr Gly Phe Ser Pro Arg Gln
    130   135   140

Ile Gln Val Ser Trp Leu Arg Glu Gly Lys Gln Val Gly Ser Gly Val
145   150   155   160

Thr Thr Asp Gln Val Gln Ala Glu Ala Lys Glu Ser Gly Pro Thr Thr
                165   170   175

Tyr Lys Val Thr Ser Thr Leu Thr Ile Lys Glu Ser Asp Trp Leu Ser
        180   185   190

Gln Ser Met Phe Thr Cys Arg Val Asp His Arg Gly Leu Thr Phe Gln
        195   200   205

Gln Asn Ala Ser Ser Met Cys Val Pro Asp Gln Asp Thr Ala Ile Arg
        210   215   220

Val Phe Ala Ile Pro Pro Ser Phe Ala Ser Ile Phe Leu Thr Lys Ser
225   230   235   240

Thr Lys Leu Thr Cys Leu Val Thr Asp Leu Thr Thr Tyr Asp Ser Val
            245   250   255

Thr Ile Ser Trp Thr Arg Gln Asn Gly Glu Ala Val Lys Thr His Thr
           260   265   270

Asn Ile Ser Glu Ser His Pro Asn Ala Thr Phe Ser Ala Val Gly Glu
        275   280   285

Ala Ser Ile Cys Glu Asp Asp Trp Asn Ser Gly Glu Arg Phe Thr Cys
        290   295   300

Thr Val Thr His Thr Asp Leu Pro Ser Pro Leu Lys Gln Thr Ile Ser
305   310   315   320

Arg Pro Lys Gly Val Ala Leu His Arg Pro Asp Val Tyr Leu Leu Pro
           325   330   335

Pro Ala Arg Glu Gln Leu Asn Leu Arg Glu Ser Ala Thr Ile Thr Cys
        340   345   350

Leu Val Thr Gly Phe Ser Pro Ala Asp Val Phe Val Gln Trp Gln Met
        355   360   365

Gln Arg Gly Gln Pro Leu Ser Pro Glu Lys Tyr Val Thr Ser Ala Pro
        370   375   380

Met Pro Glu Pro Gln Ala Pro Gly Arg Tyr Phe Ala His Ser Ile Leu
385   390   395   400

Thr Val Ser Glu Glu Glu Trp Asn Thr Gly Glu Thr Tyr Thr Cys Val
           405   410   415

Val Ala His Glu Ala Leu Pro Asn Arg Val Thr Glu Arg Thr Val Asp

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          420                425                430
```

Lys Ser Thr Gly Lys Pro Thr Ser Ala Asp Glu Glu Gly Phe Glu Asn
         435   440   445

Leu Trp Ala Thr Ala Ser Thr Phe Ile Val Leu Tyr Asn Val Ser Leu
    450   455   460

Val Met Ser Asp Thr Ala Gly Thr Cys Tyr Val Lys
465   470   475

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<212>   PRT
<213>   Homo sapiens

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<223>   Light chain kappa constant region (IgKc)

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Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
1   5   10   15

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
         20   25   30

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
         35   40   45

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
    50   55   60

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
65   70   75   80

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
         85   90   95

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
         100   105

<210>   41
<211>   107
<212>   PRT
<213>   Homo sapiens

<220>

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<223>   Light chain lambda constant region (IgLambda)

<400>   41

Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser
1               5                   10                  15

Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp
            20                  25                  30

Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro
        35                  40                  45

Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn
    50                  55                  60

Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys
65                  70                  75                  80

Ser His Arg Lys Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr
                85                  90                  95

Val Glu Lys Thr Val Ala Pro Thr Glu Cys Ser
                100                 105


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<213>   Homo sapiens


<220>
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<223>   heavy chain (HC) complementary determining region (CDR) 1

<400>   42

Asp His Tyr Val His
1               5


<210>   43
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<220>
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<223>   HC CDR 2

<400>   43
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Trp Ile Ala Pro Lys Asn Gly Tyr Ser Glu Ser Ala Pro Lys Phe Gln
1   5   10   15

Gly

<210> 44
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<212> PRT
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<220>
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<223> HC CDR 3

<400> 44

Gly Phe Tyr Asp Ser Ser Leu Tyr
1   5

<210> 45
<211> 16
<212> PRT
<213> Homo sapiens

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<223> light chain (LC) complementary determining region (CDR) 1

<400> 45

Lys Ser Gly Gln Ser Leu Leu Ala Arg Asp Gly Lys Thr Tyr Leu Ser
1   5   10   15

<210> 46
<211> 7
<212> PRT
<213> Homo sapiens

<220>
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<223> LC CDR 2

<400> 46

Leu Val Ser Lys Leu Asp Ser
1   5

<210> 47
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<212> PRT

<213>   Homo sapiens

<220>
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<223>   LC CDR 3

<400>   47

Trp Gln Gly Thr His Phe Pro Arg Thr
1   5

<210>   48
<211>   136
<212>   PRT
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<223>   CDR 1

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<223>   FR 2

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<223>   CDR 2

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<223>   FR 3

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<222>   (118)..(125)
<223>   CDR 3

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<223>   FR4/J region

<400>   48

Met Lys Cys Ser Trp Val Ile Phe Phe Leu Met Ala Val Val Ile Gly

1   5   10   15

Ile Asn Ser Glu Gly Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg
            20   25   30

Ser Gly Ala Ser Leu Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile
            35   40   45

Lys Asp His Tyr Val His Trp Val Arg Gln Arg Pro Glu Gln Gly Leu
    50   55   60

Asp Trp Ile Gly Trp Ile Ala Pro Lys Asn Gly Tyr Ser Glu Ser Ala
65   70   75   80

Pro Lys Phe Gln Gly Lys Ala Ser Met Thr Ala Asp Thr Ser Ser Asn
            85   90   95

Thr Val Tyr Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val
            100   105   110

Tyr Tyr Cys Phe Ala Gly Phe Tyr Asp Ser Ser Leu Tyr Trp Gly Gln
            115   120   125

Gly Thr Thr Leu Thr Val Ser Ser
    130   135

<210> 49
<211> 133
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<223> CDR1

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<223> FR2

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<223>  CDR2

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<223>  FR3

<220>
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<222>  (114)..(122)
<223>  CDR3

<220>
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<222>  (123)..(133)
<223>  FR4/J region

<400>  49
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Met Met Ser Pro Ala Gln Phe Leu Phe Leu Leu Val Leu Trp Ile Arg
1   5   10   15

Glu Thr Asn Gly Asp Val Val Met Thr Gln Thr Pro Leu Thr Leu Ala
                20   25   30

Val Thr Ile Gly Gln Pro Ala Ser Ile Ser Cys Lys Ser Gly Gln Ser
            35   40   45

Leu Leu Ala Arg Asp Gly Lys Thr Tyr Leu Ser Trp Leu Leu Gln Arg
    50   55   60

Pro Gly Gln Ser Pro Lys Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp
65   70   75   80

Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
                85   90   95

Thr Leu Lys Ile Asn Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr
                100   105   110

Cys Trp Gln Gly Thr His Phe Pro Arg Thr Phe Gly Gly Gly Thr Asn
                115   120   125

Leu Glu Ile Lys Arg
        130

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<213>  Homo sapiens

<220>
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<223>   Known beta amyloid sequence

<400>   50

Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys
1               5                   10                  15


Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile
            20                  25                  30


Gly Leu Met Val Gly Gly Val Val Ile Ala
            35                  40


<210>   51
<211>   408
<212>   DNA
<213>   Homo sapiens


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<223>   C701 HC

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<223>   FR1

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<222>   (148)..(162)
<223>   CDR1

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<223>   FR2

<220>
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<222>   (205)..(255)
<223>   CDR2

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<223>   FR3

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<222>   (352)..(375)
<223>   CDR3
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<223>  FR4/J Region

<400>  51
atgaaatgca gctgggtcat cttcttcctg atggcagtgg tcataggaat caattcagag      60

ggtcagctgc agcagtctgg ggcagaactt gtgaggtcag gggcctcact caagttgtcc     120

tgcacagctt ctggcttcaa tattaaagac cactatgtac actgggtgag gcagaggcct     180

gaacagggcc tggactggat tggatggatt gctccgaaga atggttatag tgaatctgcc     240

ccgaaattcc agggcaaggc cagtatgact gcagacacat cctccaacac agtctacctg     300

cagctcagca gcctgacatc tgaggacact gccgtctatt actgttttgc agggtttttac    360

gatagtagcc tctactgggg ccagggcacc actctcacag tctcttca                  408
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<210>  52
<211>  399
<212>  DNA
<213>  Homo sapiens

<220>
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<223>  FR1

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<223>  CDR1

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<222>  (178)..(222)
<223>  FR2

<220>
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<222>  (223)..(243)
<223>  CDR2

<220>
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<222>  (244)..(339)
<223>  FR3

<220>
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<222>   (340)..(366)
<223>   CDR3

<220>
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<222>   (367)..(399)
<223>   FR4/J Region

<400>   52
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gacgttgtaa tgacccagac tccactcact ttggcggtta ccattggaca accagcctcc     120

atctcttgca agtcaggtca gagcctctta gcaagagatg gaaagacata tttgagttgg     180

ttattacaga ggccaggcca gtctccaaag cgcctaatct atctggtgtc taaactggac     240

tctggagtcc ctgacaggtt ctctggcagt ggatcaggga cagatttcac actgaaaatc     300

aacagagtgg aggctgagga tttgggagtt tattattgct ggcaaggtac acattttcct     360

cggacgttcg gtggaggcac caacctggaa atcaaacgg                            399


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<220>
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<223>   HC CDR1

<400>   53

Thr Ser Gly Met Gly Val Ser
1               5


<210>   54
<211>   16
<212>   PRT
<213>   Homo sapiens


<220>
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<223>   HC CDR2

<400>   54

His Ile Tyr Trp Asp Asp Asp Lys Arg Tyr Asn Pro Ser Leu Lys Ser
1               5                   10                  15


<210>   55
<211>   13
<212>   PRT
<213>   Homo sapiens
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<223>  HC CDR3

<400>  55
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Ser Ser Gly Ser Ile Val Ile Ala Thr Gly Phe Ala Tyr
1               5                   10
```

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<210>  56
<211>  16
<212>  PRT
<213>  Homo sapiens
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<220>
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<222>  (1)..(16)
<223>  LC CDR1

<400>  56
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Arg Ser Ser Gln Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu Glu
1               5                   10                  15
```

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<210>  57
<211>  7
<212>  PRT
<213>  Homo sapiens
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<220>
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<400>  57
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```
Lys Val Ser Asn Arg Phe Ser
1               5
```

```
<210>  58
<211>  9
<212>  PRT
<213>  Homo sapiens
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<220>
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<222>  (1)..(9)
<223>  LC CDR3

<400>  58
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```
Phe Gln Gly Ser Arg Val Pro Leu Thr
1               5
```

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<210>  59
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<213>  Homo sapiens


<220>
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<223>  C705 HC

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<220>
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<223>  FR1

<220>
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<223>  CDR2

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<223>  CDR3

<220>
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<223>  FR4/J Region

<400>  59
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Met Asp Arg Leu Thr Ser Ser Phe Leu Leu Leu Ile Val Pro Ala Tyr
1   5   10   15

Val Leu Ser Gln Val Thr Leu Lys Glu Ser Gly Pro Gly Ile Leu Gln
            20   25   30

Pro Ser Gln Thr Leu Ser Leu Thr Cys Ser Phe Ser Gly Phe Ser Leu
        35   40   45

Ser Thr Ser Gly Met Gly Val Ser Trp Ile Arg Gln Pro Ser Gly Lys
        50   55   60

Gly Leu Glu Trp Leu Ala His Ile Tyr Trp Asp Asp Asp Lys Arg Tyr
65   70   75   80

Asn Pro Ser Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Arg
                85   90   95

Asn Gln Val Phe Leu Lys Ile Thr Ser Val Asp Thr Thr Asp Thr Ala
            100   105   110

Thr Tyr Tyr Cys Thr Arg Ser Ser Gly Ser Ile Val Ile Ala Thr Gly
        115   120   125

Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala
    130   135   140

<210> 60
<211> 132
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<213> Homo sapiens

<220>
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<223> FR2

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<223> CDR2

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<223> FR3

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<223> CDR3

<220>
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<223> FR4/J Region

<400> 60

Met Lys Leu Pro Val Arg Leu Leu Val Leu Met Phe Trp Ile Pro Gly
1   5   10   15

Ser Ser Ser Asp Val Met Met Thr Gln Thr Pro Leu Ser Leu Pro Val
            20   25   30

Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu
            35   40   45

Val His Ser Asn Gly Asn Thr Tyr Leu Glu Trp Tyr Met Gln Lys Pro
        50   55   60

Gly Gln Ser Pro Met Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser
65   70   75   80

Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
                85   90   95

Leu Lys Ile Ser Ser Val Glu Ala Glu Asp Leu Gly Val Phe Tyr Cys
            100   105   110

Phe Gln Gly Ser Arg Val Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu
            115   120   125

Glu Leu Lys Arg
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tgttctttct ctgggttttc actgagcact tctggtatgg gtgtgagctg gattcgtcag   180

ccttcaggaa agggtctgga gtggctggca cacatttact gggatgatga caaacgatat   240

aatccatccc tgaagagccg gctcacaatc tccaaggata cttccagaaa ccaggtattc   300

ctcaagatca ccagtgtgga cactacagat actgccacat actactgtac tcgaagttcc   360

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tcttgcagat ctagtcagag tcttgtacat agtaatggaa acacctattt agaatggtat   180

atgcagaaac caggccagtc tccaatgctc ctgatctaca agtttccaa ccgattttct    240

ggggtcccag acaggttcag tggcagtgga tcagggacag atttcacact caagatcagc   300

agcgtggagg ctgaggatct gggagttttt tactgctttc aaggttcacg tgttccgctc   360

acgttcggtg ctgggaccaa gctggagctg aaacgg                            396


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Gly
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Glu Gly Ser Asn Asn Asn Ala Leu Ala Tyr
1               5                   10
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Ser Ala Ser Ser Ser Val Ser Tyr Met His
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Asp Ser Ser Arg Leu Ala Ser
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Gln Asn Trp Arg Ser Ser Pro Thr
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<223>   FR4/J Region

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Met Glu Trp Thr Trp Val Phe Leu Phe Leu Leu Ser Val Thr Ala Gly
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Val His Ser Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Met Lys
            20   25   30

Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Thr Gly Tyr Thr Phe
            35   40   45

Ser Thr Ser Trp Ile Glu Trp Ile Lys Gln Arg Pro Gly His Gly Leu
        50   55   60

Glu Trp Ile Gly Glu Val Leu Pro Gly Ser Gly Lys Ser Asn His Asn
65   70   75   80

Ala Asn Phe Lys Gly Arg Ala Thr Phe Thr Ala Asp Thr Ala Ser Asn
                85   90   95

Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val
                100   105   110

Tyr Tyr Cys Ala Arg Glu Gly Ser Asn Asn Asn Ala Leu Ala Tyr Trp
        115   120   125

Gly Gln Gly Thr Leu Val Thr Val Ser Ala
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1               5                  10                  15


Val Ile Ile Ser Arg Gly Gln Ile Val Leu Thr Gln Ser Pro Ala Ile
            20                  25                  30


Met Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Ser Ala Ser
        35                  40                  45
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Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Ser Gly Thr Ser
    50              55              60
```

```
Pro Lys Arg Trp Ile Tyr Asp Ser Ser Arg Leu Ala Ser Gly Val Pro
65              70              75              80
```

```
Ser Arg Phe Ser Gly Gly Gly Ser Gly Thr Ser Tyr Ser Pro Thr Ile
            85              90              95
```

```
Ser Asn Met Glu Ala Glu Asp Ala Ala Thr Tyr Phe Cys Gln Asn Trp
            100             105             110
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Arg Ser Ser Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg
            115             120             125
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tgcaaggcta ctggctacac attcagtacc tcctggatag agtggataaa gcagaggcct   180

ggacatggcc ttgagtggat tggagaggtc ttacctggaa gcggtaagag taaccacaat   240

gcgaacttta agggcagggc cacatttact gcagatacag cctccaacac agcctacatg   300

cagctcagca gcctgacatc tgaggactct gccgtctatt attgtgcaag agaggggagt   360

aataacaacg ctttggctta ctggggccaa gggactctgg tcactgtctc tgca          414


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gtcaccatga cctgcagtgc cagctcaagt gtgagttaca tgcactggta ccaacagaag   180

tcaggcacct cccccaaaag atggatttat gacagttcca gactggcttc tggagtccct   240

tctcgcttca gtggcggtgg gtctgggacc tcttactctc ccacaatcag caacatggag   300

gctgaagatg ctgccacgta tttctgccag aactggcgta gtagccccac gttcggtgct   360

gggaccaagc tggagctgaa acgg   384

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Glu Tyr Ile Met Ser
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Ser Ile Asn Pro Asn Thr Gly Gly Ser Arg Tyr Asn Gln Lys Phe Lys
1   5   10   15

Gly

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Gly Asp Phe Asp Tyr
1   5

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Arg Ser Ser Lys Asn Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr
1   5   10   15

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Arg Val Ser Asn Leu Ala Ser
1   5

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Ala Gln Leu Leu Glu Leu Pro Phe Thr
1   5

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Val Leu Ser Glu Val Gln Leu Gln Gln Ser Gly Pro Asp Leu Val Lys
                20   25   30

Pro Gly Ala Ser Val Lys Thr Ser Cys Lys Thr Ser Gly Tyr Ser Phe
            35   40   45

Thr Glu Tyr Ile Met Ser Trp Val Arg Gln Ser His Gly Lys Ser Leu
    50   55   60

Glu Trp Ile Gly Ser Ile Asn Pro Asn Thr Gly Gly Ser Arg Tyr Asn
65   70   75   80

Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser
                85   90   95

Thr Ala Tyr Met Glu Phe Arg Ser Leu Thr Ser Glu Asp Ser Ala Val
                100   105   110

Tyr Tyr Cys Ala Arg Gly Asp Phe Asp Tyr Trp Gly Gln Gly Thr Thr
            115   120   125

Leu Thr Val Ser Ser
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Met Arg Phe Ser Ala Gln Leu Leu Gly Leu Leu Val Leu Trp Ile Pro
1   5   10   15

Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ala Ala Phe Ser Asn Pro
            20   25   30

Val Thr Leu Gly Thr Ser Ala Ser Ile Ser Cys Arg Ser Ser Lys Asn
        35   40   45

Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Arg
    50   55   60

Pro Gly Gln Ser Pro Gln Leu Leu Ile Ser Arg Val Ser Asn Leu Ala
65   70   75   80

Ser Gly Val Pro Asn Arg Phe Ser Gly Ser Glu Ser Gly Thr Asp Phe
                85   90   95

Thr Leu Arg Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
            100   105   110

Cys Ala Gln Leu Leu Glu Leu Pro Phe Thr Phe Gly Ser Gly Thr Lys
    ·115   120   125

Leu Glu Ile Lys Arg
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tgcaagactt ctggatactc attcactgaa tacatcatga gctgggtgag gcagagccat     180

ggaaagagcc ttgagtggat tggaagtatt aatcctaaca ctggtggtag tagatacaac     240

cagaaattca gggcaaggc cacgttgact gtagataagt cctccagcac agcctacatg     300

gagtttcgca gcctgacatc tgaggattct gcagtctatt actgtgcaag aggggacttt     360

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atctcctgca ggtctagtaa gaatctccta catagtaatg gcatcactta tttgtattgg   180

tatctgcaga ggccaggcca gtctcctcag ctcctgatat ctcgggtgtc caatctggcc   240

tcaggagtcc caaacaggtt cagtggcagt gagtcaggaa ctgatttcac actgagaatc   300

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<400> 83

Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His
1   5   10

<210> 84
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<400> 84

Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His
1   5   10

<210> 85
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<400> 85

Ile Ile Gly Leu Met Val Gly Gly Val Val Ile Ala
1   5   10

<210> 86
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<400> 86

Ile Gly Leu Met Val Gly Gly Val Val Ile Ala
1   5   10

<210> 87
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<212> PRT
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<220>
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<400> 87

Ile Gly Leu Met Val Gly Gly Val Val Ile
1   5   10

<210> 88
<211> 9
<212> PRT
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<220>
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<400> 88

Ile Gly Leu Met Val Gly Gly Val Val
1   5

<210> 89
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Ile Gly Leu Met Val Gly Gly Val
1   5

<210> 90
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1   5

<210> 91
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Leu Met Val Gly Gly Val
1   5

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Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln
1   5   10   15

<210> 93
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Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln
1   5   10

<210> 94
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Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His
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Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys Leu
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Lys Gly Ala Ile Ile Gly Leu Met Val Gly
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Glu Val His His Gln Lys Leu
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Ser Gly Tyr Glu Val His
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Gly Val Val Ile Ala Thr
1   5